

SEQUENCE LISTING

<110> Carter Holt Harvey Limited
Tasman Biotechnology Limited
Michigan Technological University
Podila, Gopi Krishna
Liu, Jun-Jun
Karnosky, David F

<120> Plants Having Modified Reproductive Activity

<130> 25635 MRB

<140>
<141>

<150> NZ334715

<151> 1999-03-17

<160> 17

<170> PatentIn Ver. 2.1

<210> 1
<211> 1320
<212> DNA
<213> Pinus radiata

<400> 1
aaactcgaca gcaaatatga ttttagattat gacctagaaa taagcatagc attaaaggcat 60
atacataaca agcggtgata tactctgact gccactgtac ttgaggaaag gtagtggact 120
ctgctcaggta cattttttt ggtaagggtt gcttggcttc tggtaatata gagaagtaaa 180
gaagtaaaag gtatggact ctatcaagt acattggatt gcctttgtcg gggcttggat 240
ggcttgggtt cgtgtgagaa gccaacaatt tataagaaat atataaaata aaaaataaaaa 300
aaatttaagt gttggaaagtg aaaacggtgg ggcagaaata tacacagaag agtactttaa 360
caatgcgca ccaaggcaga ttcacaactt gatttctgga cctcgaatac gagataatgg 420
tggtaagaaa taaaggaaga gtggagtgc tttgaaaatg aatggagagc gcacaaaatg 480
gaggacgaat aaatgaaata taatgcaga gtgcatttcc ctattatttc cagaaatgt 540
tatgtgggtt cgccattcac atgggggtcg cattcagggg gtgtcatagc ggtccttga 600
ttgcagtgtg ggagttgca catgtaccaa caaatccatt catccaaaaa cctaaattta 660
tcctctccat tactattacc tacacctata ccttagtaat atgtcctgcc ttgttaactcc 720
tccactgcct gcacacgtct tagtcaatcc atctgccttc aaataggcat tattttgttc 780
tttccccctcc gactgaaagg ctatcgaccg accgaccgct catcttcttc ttctgcgca 840
ttttttctgc tggatcatca tcattaccat catcgccatc cccaccatca tcatcatgtat 900
ggtatctcta tctctccctg gcaatcgatt gttagaggaaa ggaagaggga agggggcatat 960
gtattgtatca acctacccga aaaaacaatc tgatcagccc tgctcaatct tgcttataaa 1020
tctcttatcc actgttcaat cattcagggtt tcttcccact ttcaagcaaa ggcgccccgga 1080
ttggccgtgt tcttagattt tcaggtactt aaatggacaa tattccccac ctgaagccgt 1140

tctgaaaaag atttgttgt agaaacaaaac gattgtataa tttgcttaag ttgagcttaa 1200
 ggggtttggt acctaacttg cttgtggtt atttgtttct cagaactcgg gtcgcgtcca 1260
 actgttagaa cgaaccagca caaggggttg cagctttgc tggtgctgtt gcgcatttgc 1320

<210> 2
<211> 1401
<212> DNA
<213> Pinus radiata

<400> 2
aaactcgaca gcaaatatga ttttagattat gacctagaaa taagcatagc attaaaggcat 60
atacataaca agcgtgata tactctgact gccactgtac ttgaggaaag gtagtggact 120
ctgctcaggc acattagttt ggttaagggtt gcttggcttc tggtaataat gagaagtaaa 180
gaagtaaaag gtatttgact ctagtcaagt acattggatt gccttgcg gggcttggat 240
ggcttgggtt cgtgtgagaa gccaacaatt tataagaaat atataaaata aaaaataaaaa 300
aaatttaagt gtttggaaatg aaaacggtgg ggcagaaaata tacacagaag agtactttaa 360
caatgcgcaa ccaaggcaga ttcacaactt gatttctgga cctcgaatac gagataatgg 420
ttgttaagaaa taaaggaaga gtggagtgca tttgaaaatg aatggagagc gcacaaaatg 480
gaggacgaat aaatgaaata taatgcaaga gtgcatttcc ctattatttc cagaaatgta 540
tatgtggggtt cgccatttc acatggcgatc cattcagggg gtgtcatagc ggtccttgc 600
ttgcagtgtt ggagttgcaaa catgtaccaa caaatccatt catccccaaa cctaaattt 660
tcctctccat tactattacc tacacctata cctagtaaat atgtcctgccc ttgttaactcc 720
tccactgcct gcacacgtct tagtcaatcc atctgccttc aaataggcat tattttgttc 780
tttccccctcc gactgaaagg ctatcgaccg accgaccgct catctcttc ttctgcgcaa 840
tttttctgc tggatcatca tcattaccat catcgccatc cccaccatca tcatcatgat 900
gttatctcta tctctccctg gcaatcgatt gttagggaaa ggaagaggaa aggggcataat 960
gtattgatca acctacccga aaaaacaatc tgatcagccc tgctcaatct tgcttataaaa 1020
tctcttatacc actgttcaat cattcagggtt tcttcccact ttcaagcaaa ggcgcgggaa 1080
ttggccgtgt tcttagattt tcaggtactt aaatggacaa tattccccac ctgaagccgt 1140
tctgaaaaag atttgttgtt agaaacaaaac gattgtataa tttgcttaag ttgagcttaa 1200
ggggtttggt acctaacttg cttgtggttt atttgtttct cagaactcgg gtcgcgtcca 1260
actgttagaa cgaaccagca caaggggttg cagctttgc tggtgctgtt gcgcatttgc 1320
cttttggact ggtatttagta gttgcagctt tggttgcatt acgctgtgag gatctgtgca 1380
cgaaaatttt gtgtacaaat c 1401

<210> 3
<211> 909
<212> DNA
<213> Pinus radiata

<220>
<221> CDS
<222> (1)..(669)
<223> Pinus radiata MADS box protein mRNA, complete cds

<300>

<301> Jun-Jun, Liu
 Podila, G K.
<302> Not applicable
<303> Direct submission
<304> -
<305> -
<306> ---
<307> 1997-09-09
<308> Genebank AF023615
<309> 1999-01-26
<313> 1 TO 909

<400> 3

atg	ggt	cgt	ggg	aag	att	gag	ata	aag	agg	att	gaa	aat	act	acg	aac	48
Met	Gly	Arg	Gly	Lys	Ile	Glu	Ile	Lys	Arg	Ile	Glu	Asn	Thr	Thr	Asn	
1															15	

cga	cag	gtc	act	ttc	tgc	aag	cgc	cga	aat	ggt	tta	tta	aag	aag	gcg	96
Arg	Gln	Val	Thr	Phe	Cys	Lys	Arg	Arg	Asn	Gly	Leu	Leu	Lys	Lys	Ala	
20															30	

tat	gaa	tta	tca	gtt	ctt	tgt	gat	gca	gaa	gtg	gcc	ctc	atc	gtc	ttc	144
Tyr	Glu	Leu	Ser	Val	Leu	Cys	Asp	Ala	Glu	Val	Ala	Leu	Ile	Val	Phe	
35															45	

tcc	agc	aga	ggg	aga	ctt	tat	gaa	ttt	gcc	aac	cac	agc	gtg	aag	agg	192
Ser	Ser	Arg	Gly	Arg	Leu	Tyr	Glu	Phe	Ala	Asn	His	Ser	Val	Lys	Arg	
50															60	

acg	att	gag	agg	tac	aag	aag	act	tgc	gtt	gac	aac	aac	cac	gga	ggg	240
Thr	Ile	Glu	Arg	Tyr	Lys	Lys	Thr	Cys	Val	Asp	Asn	Asn	His	Gly	Gly	
65															80	

gcg	ata	tca	gag	tcc	aat	tct	cag	tat	tgg	caa	cag	gag	gct	ggg	aaa	288
Ala	Ile	Ser	Glu	Ser	Asn	Ser	Gln	Tyr	Trp	Gln	Gln	Glu	Ala	Gly	Lys	
85															95	

ctc	aga	caa	cag	att	gac	att	ttg	caa	aat	gca	aat	agg	cat	ttg	atg	336
Leu	Arg	Gln	Gln	Ile	Asp	Ile	Leu	Gln	Asn	Ala	Asn	Arg	His	Leu	Met	
100															110	

ggt	gac	ggg	ctt	aca	gct	ttg	aac	att	aag	gaa	ctc	aag	caa	ctt	gag	384
Gly	Asp	Gly	Leu	Thr	Ala	Leu	Asn	Ile	Lys	Glu	Leu	Lys	Gln	Leu	Glu	
115															125	

gtt	cga	ctt	gaa	aaa	gga	atc	agc	cga	gtg	cga	tcc	aaa	aag	aac	gag	432
Val	Arg	Leu	Glu	Lys	Gly	Ile	Ser	Arg	Val	Arg	Ser	Lys	Lys	Asn	Glu	
130															140	

atg ttg ctt gaa gag atc gac atc atg cag aga agg gaa cac ata ctt 480
 Met Leu Leu Glu Glu Ile Asp Ile Met Gln Arg Arg Glu His Ile Leu
 145 150 155 160

atc cag gag aat gag att ctt cgc agc aag ata gcc gag tgt cag aat 528
 Ile Gln Glu Asn Glu Ile Leu Arg Ser Lys Ile Ala Glu Cys Gln Asn
 165 170 175

agc cac aac acg aac atg tta tca gct ccg gaa tat gat gca ctg ccc 576
 Ser His Asn Thr Asn Met Leu Ser Ala Pro Glu Tyr Asp Ala Leu Pro
 180 185 190

gca ttc gac tct cga aat ttc cta cat gca aat cta atc gat gcg gcc 624
 Ala Phe Asp Ser Arg Asn Phe Leu His Ala Asn Leu Ile Asp Ala Ala
 195 200 205

cat cac tat gca cat cag gaa caa aca acg ctt cag ctt ggc tga 669
 His His Tyr Ala His Gln Glu Gln Thr Thr Leu Gln Leu Gly
 210 215 220

acgttgaagc ggtggacgct taaaactcaa tcaaggcacc cgaaaaatata gctagtaacc 729

ttgaatgaga ttcagagtcg aaatattgcg aggcaagagc acaatggaag agatagctcc 789

tagtatgaat atggatttat gatattaaca tatggtttgt cagcttaaa tatagctgtt 849

tgaaacaaag aatacaacat attagctagt attttttgg cgcatgttat cttctgttg 909

<210> 4
<211> 222
<212> PRT
<213> Pinus radiata

<400> 4
Met Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr Asn
1 5 10 15
Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
20 25 30
Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe
35 40 45
Ser Ser Arg Gly Arg Leu Tyr Glu Phe Ala Asn His Ser Val Lys Arg
50 55 60
Thr Ile Glu Arg Tyr Lys Lys Thr Cys Val Asp Asn Asn His Gly Gly
65 70 75 80
Ala Ile Ser Glu Ser Asn Ser Gln Tyr Trp Gln Gln Glu Ala Gly Lys
85 90 95

Leu Arg Gln Gln Ile Asp Ile Leu Gln Asn Ala Asn Arg His Leu Met
100 105 110
Gly Asp Gly Leu Thr Ala Leu Asn Ile Lys Glu Leu Lys Gln Leu Glu
115 120 125
Val Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn Glu
130 135 140
Met Leu Leu Glu Glu Ile Asp Ile Met Gln Arg Arg Glu His Ile Leu
145 150 155 160
Ile Gln Glu Asn Glu Ile Leu Arg Ser Lys Ile Ala Glu Cys Gln Asn
165 170 175
Ser His Asn Thr Asn Met Leu Ser Ala Pro Glu Tyr Asp Ala Leu Pro
180 185 190
Ala Phe Asp Ser Arg Asn Phe Leu His Ala Asn Leu Ile Asp Ala Ala
195 200 205
His His Tyr Ala His Gln Glu Gln Thr Thr Leu Gln Leu Gly
210 215 220

<210> 5

<211> 1012

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (16)..(795)

<223> *Arabidopsis thaliana* ribonuclease (RNS2) mRNA,
complete cds

<300>

<301> Taylor, C B.

Bariola, P A.

delCardayre, S B.

Raines, R T.

Green, P J.

<302> RNS2: a senescence-associated RNase of *Arabidopsis* that
diverged from the S-RNases before speciation

<303> Proc. Natl. Acad. Sci. U.S.A.

<304> 90

<305> 11

<306> 5118-5122

<307> 1993

<308> Genbank

<309> 1994-10-30

<313> 1 TO 1012

<400> 5

atcgaattaa agtca atg gcg tca cgt tta tgt ctt ctc ctt ctc gtt gcg 51
 Met Ala Ser Arg Leu Cys Leu Leu Leu Val Ala
 1 5 10

tgt atc gcc gga gca ttt gcc gga gac gtc atc gaa ctc aat cga tct 99
 Cys Ile Ala Gly Ala Phe Ala Gly Asp Val Ile Glu Leu Asn Arg Ser
 15 20 25

cag agg gag ttc gat tat ttc gct cta tct ctt caa tgg cct gga acc 147
 Gln Arg Glu Phe Asp Tyr Phe Ala Leu Ser Leu Gln Trp Pro Gly Thr
 30 35 40

tat tgc cgt gga act cgc cat tgt tgc tcc aaa aac gct tgc tgc aga 195
 Tyr Cys Arg Gly Thr Arg His Cys Cys Ser Lys Asn Ala Cys Cys Arg
 45 50 55 60

ggc tcc gat gct cca act caa ttc aca att cat ggg tta tgg cct gac 243
 Gly Ser Asp Ala Pro Thr Gln Phe Thr Ile His Gly Leu Trp Pro Asp
 65 70 75

tat aac gat ggt tcg tgg cct tca tgt tgt tat cga tct gac ttt aaa 291
 Tyr Asn Asp Gly Ser Trp Pro Ser Cys Cys Tyr Arg Ser Asp Phe Lys
 80 85 90

gag aag gag att tca acg ttg atg gat ggt ctt gag aag tac tgg cct 339
 Glu Lys Glu Ile Ser Thr Leu Met Asp Gly Leu Glu Lys Tyr Trp Pro
 95 100 105

agt ctc agt tgt ggt tct cca tca tca tgc aat ggt ggg aaa ggg tca 387
 Ser Leu Ser Cys Gly Ser Pro Ser Ser Cys Asn Gly Lys Gly Ser
 110 115 120

ttt tgg ggc cac gag tgg gag aaa cat ggg act tgt tct tct cct gtt 435
 Phe Trp Gly His Glu Trp Glu Lys His Gly Thr Cys Ser Ser Pro Val
 125 130 135 140

ttt cat gat gag tat aat tac ttc ctt acc aca ctt aat ctc tac ttg 483
 Phe His Asp Glu Tyr Asn Tyr Phe Leu Thr Thr Leu Asn Leu Tyr Leu
 145 150 155

aag cat aat gtc acg gat gtc ctt tat caa gct ggc tat gtt gct tcc 531
 Lys His Asn Val Thr Asp Val Leu Tyr Gln Ala Gly Tyr Val Ala Ser
 160 165 170

aac agt gaa aag tat cct cta gga ggt atc gta aca gcc att cag aat 579
 Asn Ser Glu Lys Tyr Pro Leu Gly Gly Ile Val Thr Ala Ile Gln Asn
 175 180 185

gca ttt cat atc acc cct gaa gtg gtt tgc aaa aga gat gca atc gat 627
 Ala Phe His Ile Thr Pro Glu Val Val Cys Lys Arg Asp Ala Ile Asp
 190 195 200

gaa ata cgt ata tgc ttc tat aaa gat ttt aag ccc agg gac tgt gtt 675
 Glu Ile Arg Ile Cys Phe Tyr Lys Asp Phe Lys Pro Arg Asp Cys Val
 205 210 215 220

ggt tca caa gat ttg aca tct aga aag tca tgc ccc aag tac gta agt 723
 Gly Ser Gln Asp Leu Thr Ser Arg Lys Ser Cys Pro Lys Tyr Val Ser
 225 230 235

ttg ccg gaa tac acg cca tta gat ggt gaa gct atg gtt ctg aag atg 771
 Leu Pro Glu Tyr Thr Pro Leu Asp Gly Glu Ala Met Val Leu Lys Met
 240 245 250

cca aca gaa aga gaa gct ctt tga atcggaaaaag atgggagctt tgtttatcttc 825
 Pro Thr Glu Arg Glu Ala Leu
 255 260

tgagagacaa tacatacatg tctctgatgt tgtaacttta ctacaaaaac ctataaagat 885
 tggcttattt cggtctattt gatatgtatc atcattactg gtaaatcaag tttctttcta 945

ataatgtaga agatcagaaa atccataaga agatatcaac atttgagttc tatggtaaaa 1005

aaaaaaaaaa 1012

<210> 6
 <211> 259
 <212> PRT
 <213> *Arabidopsis thaliana*

<400> 6
 Met Ala Ser Arg Leu Cys Leu Leu Leu Val Ala Cys Ile Ala Gly
 1 5 10 15
 Ala Phe Ala Gly Asp Val Ile Glu Leu Asn Arg Ser Gln Arg Glu Phe
 20 25 30
 Asp Tyr Phe Ala Leu Ser Leu Gln Trp Pro Gly Thr Tyr Cys Arg Gly
 35 40 45
 Thr Arg His Cys Cys Ser Lys Asn Ala Cys Cys Arg Gly Ser Asp Ala
 50 55 60
 Pro Thr Gln Phe Thr Ile His Gly Leu Trp Pro Asp Tyr Asn Asp Gly
 65 70 75 80
 Ser Trp Pro Ser Cys Cys Tyr Arg Ser Asp Phe Lys Glu Lys Glu Ile
 85 90 95
 Ser Thr Leu Met Asp Gly Leu Glu Lys Tyr Trp Pro Ser Leu Ser Cys

100	105	110
Gly Ser Pro Ser Ser Cys Asn Gly	Gly Lys Gly Ser Phe Trp Gly His	
115	120	125
Glu Trp Glu Lys His Gly Thr Cys Ser Ser Pro Val Phe His Asp Glu		
130	135	140
Tyr Asn Tyr Phe Leu Thr Thr Leu Asn Leu Tyr Leu Lys His Asn Val		
145	150	155
Thr Asp Val Leu Tyr Gln Ala Gly Tyr Val Ala Ser Asn Ser Glu Lys		
165	170	175
Tyr Pro Leu Gly Gly Ile Val Thr Ala Ile Gln Asn Ala Phe His Ile		
180	185	190
Thr Pro Glu Val Val Cys Lys Arg Asp Ala Ile Asp Glu Ile Arg Ile		
195	200	205
Cys Phe Tyr Lys Asp Phe Lys Pro Arg Asp Cys Val Gly Ser Gln Asp		
210	215	220
Leu Thr Ser Arg Lys Ser Cys Pro Lys Tyr Val Ser Leu Pro Glu Tyr		
225	230	235
Thr Pro Leu Asp Gly Glu Ala Met Val Leu Lys Met Pro Thr Glu Arg		
245	250	255
Glu Ala Leu		

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<220>

<221> modified_base

<222> (3)

<223> i

<220>

<221> modified_base

<222> (6)

<223> i

<220>

<221> modified_base

<222> (9)

<223> i

<220>

<221> modified_base

<222> (12)

<223> i

<220>

<221> modified_base

<222> (15)

<223> i

<400> 7

gcngtnagny cntcnccat

20

<210> 8

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<220>

<221> modified_base

<222> (6)

<223> i

<220>

<221> modified_base

<222> (12)

<223> i

<220>

<221> modified_base

<222> (15)

<223> i

<400> 8

aaycgncarg tnacntt

17

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 9

cgccttcttc aataaaccat ttccggcgctt

30

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 10

gacctgtcgg ttcgttagtat tttcaatcct

30

<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 11

ttcgtcctcc attttgtgcg ctctccatcc

30

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 12

gcactccact cttcctttat ttcttaccac

30

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 13

agttacttaa caatgcgcaa ccaaggc

27

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Made in lab

<400> 14
ttgtgtacaa atcatggg

18

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Made in lab

<400> 15
gtaagcccgta caccatc

18

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Made in lab

<400> 16
gaacaagatg gattgcacgc

20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Made in lab

<400> 17

gaagaactcg tcaagaaggc

20